

## **Exhibit A**

### **Clean Version of The Pending Claims in U.S. Patent Application Ser. No. 10/041,770**

1. (Amended) An isolated nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1.
2. (Amended) An isolated nucleic acid molecule comprising a nucleotide sequence that:
  - (a) encodes the amino acid sequence shown in SEQ ID NO:2; and
  - (b) hybridizes to the nucleotide sequence of SEQ ID NO:1 or the complement thereof under highly stringent conditions of 0.5 M NaHPO<sub>4</sub>, 7% sodium dodecyl sulfate (SDS) and 1 mM EDTA at 65°C and washing in 0.1x SSC/0.1%SDS at 68°C.
3. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence described in SEQ ID NO:2.
4. (Amended) An isolated expression vector comprising a nucleic acid molecule that comprises the nucleotide sequence of SEQ ID NO:1.
5. (New) An isolated expression vector comprising a nucleic acid molecule that encodes the amino acid sequence described in SEQ ID NO:2.
6. (New) A host cell comprising the expression vector of claim 4 or 5.

## **Exhibit A**

### **Clean Version of The Pending Claims in U.S. Patent Application Ser. No. 10/041,770**

1. (Amended) An isolated nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1.
2. (Amended) An isolated nucleic acid molecule comprising a nucleotide sequence that:
  - (a) encodes the amino acid sequence shown in SEQ ID NO:2; and
  - (b) hybridizes to the nucleotide sequence of SEQ ID NO:1 or the complement thereof under highly stringent conditions of 0.5 M NaHPO<sub>4</sub>, 7% sodium dodecyl sulfate (SDS) and 1 mM EDTA at 65°C and washing in 0.1x SSC/0.1%SDS at 68°C.
3. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence described in SEQ ID NO:2.
4. (Amended) An isolated expression vector comprising a nucleic acid molecule that comprises the nucleotide sequence of SEQ ID NO:1.
5. (New) An isolated expression vector comprising a nucleic acid molecule that encodes the amino acid sequence described in SEQ ID NO:2.
6. (New) A host cell comprising the expression vector of claim 4 or 5.

## Exhibit B

### **Marked Up Version of Amended Claims in U.S. Patent Application Ser. No. 10/041,770**

1. (Amended) An isolated nucleic acid molecule comprising [at least 60 contiguous nucleotides from] the nucleotide sequence of SEQ ID NO:1.
2. (Amended) An isolated nucleic acid molecule comprising a nucleotide sequence that:
  - (a) encodes the amino acid sequence shown in SEQ ID NO:2; and
  - (b) hybridizes [under highly stringent conditions] to the nucleotide sequence of SEQ ID NO:1 or the complement thereof under highly stringent conditions of 0.5 M NaHPO<sub>4</sub>, 7% sodium dodecyl sulfate (SDS) and 1 mM EDTA at 65°C and washing in 0.1x SSC/0.1%SDS at 68°C.
3. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes the amino acid sequence described in SEQ ID NO:2.
4. (Amended) An isolated expression vector comprising a nucleic acid molecule that comprises [at least 60 contiguous nucleotides from] the nucleotide sequence of SEQ ID NO:1.
5. (New) An isolated expression vector comprising a nucleic acid molecule that encodes the amino acid sequence described in SEQ ID NO:2.
6. (New) A host cell comprising the expression vector of claim 4 or 5.

Query= SEQ ID NO:1  
(2634 letters)



Sequences producing significant alignments:

	Score (bits)	E Value
--	-----------------	------------

AL356356.17.1.176550	1386	0.0
----------------------	------	-----

>AL356356 ACCESSION:AL356356 NID: gi 18476570 emb AL356356.17 Human DNA  
sequence from clone RP11-54A4 on chromosome 1, complete  
sequence  
Length = 176550

Identities = 699/699 (100%)  
Strand = Plus / Plus

Query: 433 aggtcccggttcgagaccccatcaagccaggaatgttcggttatgggagagtgcccttt 492  
|||||  
Sbjct: 80686 aggtcccggttcgagaccccatcaagccaggaatgttcggttatgggagagtgcccttt 80745

Query: 493 gcattgccactgcaccggaaccgcaggcaccctcggagcccaccagatctgagctgtcc 552  
|||||  
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|||||  
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Identities = 360/360 (100%)  
Strand = Plus / Plus

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Query: 257 cccggcccccaagacatccagaagccctcctccccggggccaggggtccagaccccaga 316  
|||||  
Sbjct: 80338 cccggcccccaagacatccagaagccctcctccccggggccaggggtccagaccccaga 80397

Query: 317 cttctccagaaaccctccccttgtagaggacacagtctcggggaaggggtggcccacttc 376  
|||||  
Sbjct: 80398 cttctccagaaaccctccccttgtagaggacacagtctcggggaaggggtggcccacttc 80457

Query: 377 gaggtcccgccttcccacctagggagagaggagaccagagattcgagcgccaggaggt 436  
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Identities = 252/255 (98%)

Strand = Plus / Plus

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Query: 2440 aacgggtgatgaagtgcgagcaggagtgctgcgtcaggccccccacagccccccagcaga 2499  
|| |

Sbjct: 85792 aatgggtgatgaagtgcgagcaggagtgctgcgtcaggccccccacagccccccagcaga 85851

Query: 2500 gaggcctgtgacatggggccctgtactactgcctgggtccacagcgactggagctccaag 2559  
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Sbjct: 85852 gaggcctgtgacatggggccctgtactactgcctgggtccacagcgactggagctccaag 85911

Query: 2560 gtgagcccgaacccccagccatatcctgcacctgggtaaccatgccaggacacctca 2619  
|||||

Sbjct: 85912 gtgagcccgaacccccagccatatcctgcacctgggtaaccacgccaggacacctca 85971

Query: 2620 gcctttccagcatag 2634  
|||||

Sbjct: 85972 gcctttccagcatag 85986

Identities = 206/206 (100%)

Strand = Plus / Plus

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Sbjct: 83483 tgggggtgatgattctacctgtcgcttgtttcggggaacctcactgaccgagggggccc 83542

Query: 1491 cctgggctatcagaagatcttgtggattccagcgggagccttgcggtccagattgcca 1550  
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Sbjct: 83543 cctgggctatcagaagatcttgtggattccagcgggagccttgcggtccagattgcca 83602

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Sbjct: 83603 gctccggcctagctccaactacctgg 83628

Identities = 205/205 (100%)  
Strand = Plus / Plus

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Query: 2238 ccagctgcagtgccggcaggaatttgggggggggtggctcctcggtgccccggagcgctg 2297  
|||||  
Sbjct: 85267 ccagctgcagtgccggcaggaatttgggggggggtggctcctcggtgccccggagcgctg 85326

Query: 2298 tggacatctccccggcccaacatcacccagtcttgccagctgcgcctctgtggccattg 2357  
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Sbjct: 85327 tggacatctccccggcccaacatcacccagtcttgccagctgcgcctctgtggccattg 85386

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Strand = Plus / Plus

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Query: 1636 gggtcctacagggccggcgggaccgtctttcgatataaccgtcctcccagggaggagggc 1695  
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Strand = Plus / Plus

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Strand = Plus / Plus

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Query: 2106 acgcagctgtgccgcggtgccaggccccccagcctcccctgaaccctgccacggcacccc 2165  
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Sbjct: 84814 acgcagctgtgccgcggtgccaggccccccagcctcccctgaaccctgccacggcacccc 84873

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Sbjct: 84874 atgccccccata 84885

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Strand = Plus / Plus

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Strand = Plus / Plus

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Strand = Plus / Plus

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Identities = 21/21 (100%)  
Strand = Plus / Plus

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**Nucleotide**

PubMed

Nucleotide

Protein

## Genome

## Structure

PMC

## Taxonomy

OMIM

Boo

Search   for

for

for

**Go**

Clear

## Limits

[Preview/Index](#)

## History

## Clipboard

## Details

## Display

default

**Show:**

20 

**Send to**

File 

## Get Subsequence

1: AL356356. Human DNA sequenc...[gi:18476570]

## Links

```

LOCUS       AL356356                176550 bp      DNA      linear      PRI 30-JAN-2002
DEFINITION   Human DNA sequence from clone RP11-54A4 on chromosome 1, complete
              sequence.
ACCESSION    AL356356
VERSION      AL356356.17  GI:18476570
KEYWORDS     HTG.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 176550)
AUTHORS      Heath, P.
TITLE        Direct Submission
JOURNAL      Submitted (30-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
              Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
              humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT      On Feb 1, 2002 this sequence version replaced gi:18250748.
              During sequence assembly data is compared from overlapping clones.
              Where differences are found these are annotated as variations
              together with a note of the overlapping clone name. Note that the
              variation annotation may not be found in the sequence submission
              corresponding to the overlapping clone, as we submit sequences with
              only a small overlap as described above.
              This sequence was finished as follows unless otherwise noted: all
              regions were either double-stranded or sequenced with an alternate
              chemistry or covered by high quality data (i.e., phred quality >=
              30); an attempt was made to resolve all sequencing problems, such
              as compressions and repeats; all regions were covered by at least
              one plasmid subclone or more than one M13 subclone; and the
              assembly was confirmed by restriction digest. The following
              abbreviations are used to associate primary accession numbers given
              in the feature table with their source databases: Em:, EMBL; Sw:,
              SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
              database can be found at
              http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence
              was generated from part of bacterial clone contigs of human
              chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
              Group. Further information can be found at
              http://www.sanger.ac.uk/HGP/Chr1
              RP11-54A4 is from the library RPCI-11.1 constructed by the group of
              Pieter de Jong. For further details see
              http://www.chori.org/bacpac/home.htm
              VECTOR: pBACe3.6
              IMPORTANT: This sequence is not the entire insert of clone
              RP11-54A4 It may be shorter because we sequence overlapping
              sections only once, except for a short overlap.
              The true left end of clone RP11-54A4 is at 1 in this sequence. The

```

>NM\_019032 ACCESSION:NM\_019032 NID: gi 24308134 ref NM\_019032.1  
Homo sapiens thrombospondin repeat containing 1 (TSRC1),  
mRNA  
Length = 2704

Score = 950 bits (2428), Expect = 0.0  
Identities = 431/433 (99%), Positives = 431/433 (99%)  
Frame = +1

Query: 425 RGFRFYVRHTEKVQDGTLCQPGAPDICVAGRCLSPGCDGILGSGRRPDGCGVCGGDDSTC 484  
RGFRFYVRHTEKVQDGTLCQPGAPDICVAGRCLSPGCDGILGSGRRPDGCGVCGGDDSTC  
Sbjct: 1 RGFRFYVRHTEKVQDGTLCQPGAPDICVAGRCLSPGCDGILGSGRRPDGCGVCGGDDSTC 180

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Sbjct: 181 RLVSGNLTDRGGPLGYQKILWIPAGALRLQIAQLRPSSNYLALRGPGGRSIINGNWAVIDP 360

Query: 545 PGSYRAGGTVFRYNRPREEGKGESLSAEGPTTQPDVYMIFQEENPGVFYQYVISSPPP 604  
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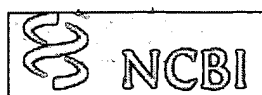
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Query: 665 AAYWKRVGHSACSASCGKGVWRPIFLCISRESGEELDERSCAAGARPPASPEPCHGTPCP 724  
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**Nucleotide**

PubMed

Nucleotide

Protein

## Genome

## Structure

PMC

## Taxonomy

OMIM

Boo

## Search

Nucleotide

for



\_\_\_\_\_

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**Go**

Clear

## Display

default

**Show:**

20

**Send to**

File 

## Get Subsequence

☐ **1:** NM\_019032[gi:24308134] This record was temporarily removed by RefSeq staff for additional review.

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VERSION     NM_019032.1   GI:24308134
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2704)
AUTHORS     Strausberg,R.
TITLE       Homo sapiens, hyothetical protein, clone MGC:34896 IMAGE:5001173,
            mRNA
JOURNAL     Unpublished (2002)
COMMENT     PROVISIONAL REFSEQ: This record has not yet been subject to final
            NCBI review. The reference sequence was derived from BC027478.1.
FEATURES             Location/Qualifiers
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BASE COUNT 510 a 873 c 774 g 547 t

ORIGIN

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```

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Jun 19 2003 12:37:45

>AY158701 ACCESSION:AY158701 NID: gi 30024980 gb AY158701.1 Mus  
musculus thrombospondin repeat protein 1 (Tsrc1) mRNA,  
complete cds  
Length = 3856

Score = 1322 bits (3383), Expect = 0.0  
Identities = 640/860 (74%), Positives = 686/860 (79%), Gaps = 3/860 (0%)  
Frame = +3

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ME+W GR WL ++LLL LPQ C DQE L G S Q P+EEGQ PEG+WGPW +WASCSQPC  
Sbjct: 117 MESWLGRLWLCMMLLLPLPQPCDQE-LFGPSHLQLPSEEGQVPEGLWGPWGRWASCSQPC 293

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Query: 121 RGGPLRG PASHLGREETQEIRAARRSRLRDPKPGMFGYGRVPFALPLHRNRRHPRSPPR 180  
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P PF VPR QQ + W P GP PD WLPL + +S LWS+FAP  
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Query: 418 CELNCRPRGRFRFYVRHTEKVQDGTLCQPGAPDICVAGRCLSPGCDGILGSGRRPDGCGVC 477  
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Query: 838 MGPCTTAWFHSDWSSKVSPE 857  
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Handwritten calculations:  
$$\begin{array}{r} 111 \\ 3 \overline{) 2162} \end{array}$$
$$\begin{array}{r} 820 \\ + 75 \\ \hline 895 \end{array}$$



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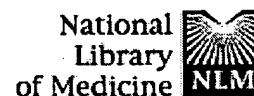
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 223  
 18 x 60 = 1080

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```

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## TSRC1, a widely expressed gene containing seven thrombospondin type I repeats.

**Buchner DA, Meisler MH.**

Department of Human Genetics, University of Michigan School of Medicine  
Ann Arbor, MI 48109-0618, USA.

The thrombospondin type 1 repeat domain is found in nearly 100 mammalian proteins with diverse biological functions that include cellular adhesion, angiogenesis, and patterning of the developing nervous system. We have characterized a novel thrombospondin type 1 repeat containing gene, TSRC1 encoding a predicted protein with seven thrombospondin repeats, six of which are clustered at the C-terminus. The 17 coding exons and two nontranslated exons of TSRC1 span 10 kb of genomic DNA. The human and mouse genes encode proteins of 1074 and 1036 amino acids, respectively, with 76% amino acid sequence identity. Thirty of the extra amino acids in the human protein are encoded by exon 6. Mouse Tsrc1 is expressed in all fetal and adult tissues tested. Three conserved noncoding sequence elements with potential regulatory function are located in intron 1. Mouse Tsrc1 was genetically mapped to chromosome 3 within the nonrecombinant region for the sodium channel modifier locus Scnm1. The sensitive and resistant alleles of Scnm1 did not differ in Tsrc1 protein sequence, transcript length, or transcript abundance. Human TSRC1 is located on chromosome 1q21 within an 11.7 Mb segment of conserved synteny. TSRC1 and the closely linked gene ADAM15 appear to have been derived by a chromosomal inversion that interrupted an ancestral ADAMTS gene.

PMID: 12706885 [PubMed - indexed for MEDLINE]

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## SMART ANALYSIS

Domains within the query sequence of 877 residues

